

## **CLAIMS**

What is claimed is:

An isolated nucleic acid sequence encoding a tocopherol cyclase.

2. An isolated nucleic acid sequence according to Claim 1, wherein said tocopherol cyclase is active in the cyclization of 2,3-dimethyl-5-phytylplastoquinol to tocopherol.

3. An isolated nucleic acid sequence according to Claim 1, wherein said tocopherol cyclase is active in the cyclization of 2,3-dimethyl-5-geranylgeranylplastoquinol to tocotrienol.

- 4. An isolated DNA sequence according to Claim 1, wherein said nucleic acid sequence is isolated from a eukaryotic cell source.
- 5. An isolated DNA sequence according to Claim 4, wherein said eukaryotic cell source is selected from the group consisting of mammalian, nematode, fungal, and plant cells.
- 6 The DNA encoding sequence of Claim 5 wherein said tocopherol cyclase protein is from *Arabidopsis*.
- 7. The DNA encoding sequence of Claim 6 wherein said tocopherol cyclase protein is encoded by a sequence of SEQ ID NO:109.
- 8. The DNA encoding sequence of Claim 7 wherein said tocopherol cyclase protein has an amino acid sequence of SEQ ID NO:110.
- 9. The DNA encoding sequence of Claim 4 wherein said tocopherol cyclase protein is from a source selected from the group consisting of *Arabidopsis*, soybean, corn, rice, wheat, leek canola, , leek, cotton, and tomato.

Synechocystis sp.

- 11. The DNA encoding sequence of Claim 10 wherein said tocopherol cyclase protein is encoded by a sequence of SEQ ID NO:38.
- 12. The DNA encoding sequence of Claim 10 wherein said tocopherol cyclase protein has an amino acid sequence of SEQ ID NO:39.
- A nucleic acid construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a nucleic acid sequence encoding a tocopherol cyclase, and a transcriptional termination region.

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- 14. A nucleic acid construct according to Claim 13, wherein said nucleic acid sequence encoding tocopherol cyclase is obtained from an organism selected from the group consisting of a eukaryotic organism and a prokaryotic organism.
- 15. A nucleic acid construct according to Claim 14, wherein said nucleic acid sequence encoding tocopherol cyclase is obtained from a plant source.
- 16. A nucleic acid construct according to Claim 15, wherein said nucleic acid sequence encoding tocopherol cyclase is obtained from a source selected from the group consisting of Arabidopsis, soybean, corn, rice, wheat, teek canola, , leek, cotton, and tomato.
- 17. A nucleic acid construct according to Claim 13, wherein said nucleic acid sequence encoding tocopherol cyclase is obtained from a Synechocystis sp.
  - 18. A plant cell comprising the construct of 13.
    - 19. A plant comprising a cell of Claim 18.
    - 20 A feed composition produced from a plant according to Claim 19.
    - 21. A seed comprising a cell of Claim 18.
    - 220 Oil obtained from a seed of Claim 21.
- 23. A natural tocopherol rich refined and deodorised oil which has been produced by a method of treating an oil according to Claim 22 by distilling under low pressure and high temperature, wherein said refined oil has reduced free fatty acids and a substantial percentage of tocopherol present in the pretreated oil.
- 24. A refined oil according to claim 23, wherein the pretreated oil is crude or pre-treated soybean oil.
- 25. A refined oil according to claim 23, wherein the refined oil is degummed and bleached.
- 26. A method for the alteration of the isoprenoid content in a host cell, said method comprising; transforming said host cell with a construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a nucleic acid sequence encoding tocopherol cyclase, and a transcriptional termination region,

wherein said isoprenoid compound selected from the group of tocopherols and tocotrienols.

27. The method according to Claim 26, wherein said host cell is selected from the group consisting of a prokaryotic cell and a eukaryotic cell.

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- 29. The method according to Claim 27, wherein said eukaryotic cell is a plant cell.
- 30. The method according to Claim 29, wherein said plant cell is obtained from a plant selected from the group consisting of *Arabidopsis*, soybean, corn, rice, wheat, leek canola, , leek, cotton, and tomato.

31. A method for producing an isoprenoid compound of interest in a host cell, said method comprising obtaining a transformed host cell, said host cell having and expressing in its genome:

a construct having a DNA sequence encoding a tocopherol cyclase operably linked to a transcriptional initiation region functional in a host cell,

wherein said isoprenoid compound selected from the group of tocopherols and tocotrienols.

- 32. The method according to Claim 31, wherein said host cell is selected from the group consisting of a prokaryotic cell and a eukaryotic cell.
  - 33. The method according to Claim 32, wherein said prokaryotic cell is a Synechocystis sp.
  - 34. The method according to Claim 32, wherein said eukaryotic cell is a plant cell.
- 35. The method according to Claim 34, wherein said plant cell is obtained from a plant selected from the group consisting wherein said compound selected from the group of *Arabidopsis*, soybean, corn, rice, wheat, leek canola, , leek, cotton, and tomato.

36. A method for increasing the biosynthetic flux in a host cell toward production of an isoprenoid compound, said method comprising;

transforming said host cell with a construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a DNA encoding a tocopherol cyclase, and a transcriptional termination region,

wherein said isoprenoid compound selected from the group of tocopherols and tocotrienols,

- 37. The method according to Claim 36, wherein said host cell is selected from the group consisting of a prokaryotic cell and a eukaryotic cell.
  - 38. The method according to Claim 37, wherein said prokaryotic cell is a Synechocystis sp.
  - 39. The method according to Claim 37, wherein said eukaryotic cell is a plant cell.

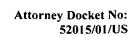
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40. The method according to Claim 39, wherein said plant cell is obtained from a plant selected from the group consisting *Arabidopsis*, soybean, corn, rice, wheat, leek canola, , leek, cotton, and tomato

41. The method according to Claim 39, wherein said transcriptional initiation region is a seed-specific promoter.

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